SEQUENCE LISTING

<110> LIBON Christine CORVAIA Nathalie N'GUYEN Thien BECK Alain BONNEFOY Jean-Yves <120> BACTERIAL MEMBRANE FRACTIONS WITH ADJUVANT EFFFECT <130> D17975 <150> FR 99 03 153 <151> 1999-03-15 <150> PCT/FR00/00622 <151> 2000-03-15 <160> 2 <170> PatentIn Vers. 2.0 <210> 1 <211> 1035 <212> DNA <213> Klebsiella pneumoniae <220> <221> exon <222> (1)..(1032) <220> <221> intron <222> (1033)..(1035) <220> <221> CDS <222> (1)..(1032) <400> 1 atg aaa gca att ttc gta ctg aat gcg gct ccg aaa gat aac acc tgg 48 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp 5 15 96 tat qca qqt qqt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe 20 tac ggt aac ggt ttc cag aac aac ggt ccg acc cgt aac gat cag 144 Tyr Gly Asn Gly Phe Gln Asn Asn Gly Pro Thr Arg Asn Asp Gln 35 ctt ggt gct ggt tcc ggt tac cag gtt aac ccg tac ctc ggt 192 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly 50 55 ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc 240 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser 65 70 75

gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa

288

Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys 336 ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly 105 ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc 384 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly 120 gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gct ggc 432 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly 135 ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac 480 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr 150 145 cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct 528 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro 170 165 gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa 576 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu 185 gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gca gtg 624 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val 200 195 gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac 672 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn 215 210 aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac 720 Lvs Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr 235 230 768 act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Leu 250 245 ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct 816 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser 260 265 gag aaa cgt gct cag tcc gtt gtt gac tac ctg gtt gct aaa ggc atc 864 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile 280 ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt 912 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val 290 295 act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat 960 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp 305 310 315 tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa 1008 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys

1035

335 330 325

gaa gtt gta act cag ccg gcg ggt taa Glu Val Val Thr Gln Pro Ala Gly

340

<210> 2 <211> 344

<212> PRT

<213> Klebsiella pneumoniae

<400> 2

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Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe

Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln

Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly

Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser

Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys

Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly 100

Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly 120

Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly 130

Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr 150

Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro 170

Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu 180

Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val

Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn 215

Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr 230

Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Leu 250 245

Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser 260 265 270

Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile 275 280 285

Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val 290 295 300

Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp 305 310 315 320

Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys 325 330 335

Glu Val Val Thr Gln Pro Ala Gly 340